

Signal Peptide		Prodomain	
DKUZ	MSSKCAFNIVFVSIIIFIIVNGYAKDISGVKRGHERLNEYISHYEITLNYDHEHIRASHNRRARRSVTK-DQYVHLK	74	
MKUZ	MVLPTVLILLSSAAGLG--QYGNPLNKYIRHYEGLSYNVDSLHQQKHQRAKRAVSHEDQFLLED	63	
DKUZ	FASHGRDFFHRLKRDNLNTFSNKLDFYDSKGPIDVSTIDHIYEGEVIIDGRNSYVFGSIHNGVFEFGKIIITERDAYVVE	149	
MKUZ	FHAHGRQFENLRMKRDTSLFSDEFKVFSTNKLVDYDTSIIYTGHIYGEESFSGSVIDGRFEGFKIRGGTFYIE	138	
DKUZ	HAKHYFPTNRTATTPPSTITSSATTVTKSTQPTRLAKSNTSTIAVNSKTENFIKKIAESTITTSQQLPEYTES	224	
MKUZ	PAERYIK-----	145	
DKUZ	SSSSSTTFPPTTEFEDEKERNAEDELDFHSIIYKESHVEDAYENVREGHVAGCGITDEVSQWMENIQNSAVEE	299	
MKUZ	-----DRILPFHSHVIYHEDDINYPHKYGPQGGCAD---HSVFERMRKYQMTGVEE	192	
Metalloprotease Domain			
DKUZ	LPEPMSKDYQKLHRKQCHKKSAAPQQQQPPPKKYISGDEDFKYPHQKYTKEANFAEGAFYDPSTGRRLGSSANV	374	
MKUZ	GARAHPEKHAASSGPELRLK-----	213	
DKUZ	ADWHQLVHERVRATDNGAGDRGSSGGSGRGREDNKNICSLYIQIDPLIWRHIREGIAADHGRKYEVEDEKTRIEE	449	
MKUZ	-----RTTLAERNTCQLYIQIDHLLFFKY-----GTREA	442	
DKUZ	ITSLIAHHVIAVNYIYRNITKFDGRTEHRNIRFEVQRITKIDDDSAACRNSYNGPHNATCNEHMDVSNFLNLHSLLEDH	524	
MKUZ	VIAQISSHVKAIDTIYQTIDESGI---RNISEFMVKRIINTISDEK---PTNPFRFPNIGVEKFLNELNSEQN	310	
DKUZ	SDFCLAYVFTYRDFITGGTGLGLAWVASAGSAGSGGICEKIKYKITYTETVGGQYQSTKRSNTIGIITFVNYNSRVPPKVS	599	
MKUZ	DDYCLAYVFTDRDFDDGVGLGLAWVGAPSGSGGICEKSKLYSD-----GKKKSLNTIGIITVQNYGSHVPPKVS	378	
Zn++			
DKUZ	QLTIAHEIGHNFGSPHDYPQECRPPGGL-----NGNYIMFAISATSGDRPNNSKFSPCSIRNINSNVL DVLVGNIK	667	
MKUZ	HITFAHEVGHNFGSPHDSGETCTPGESKNLGGKENGNYIMYARATSGDKLNNKFSLC SIRNINSQL E---KKR	449	
DKUZ	RDCKKASIEGAFCGNKIYVSGEEDCGFNEECCDKCCYPRLISEYDQSLNSSAKGCTRRAKTQCSPSQGGPCCLSN	742	
MKUZ	NNCFVESGQPICGNGMVEQGEEDCGYSDQ-CKDDCGF-----DANQPEGKKCKLKPQKQCCSPSQGGPCC-TA	514	
XKUZ	-----YSDQ-CKDECCY-----DANQPEENKCTLKPGKQCCSPSQGGPCC-TT	39	
Cysteine-rich Domain			
DKUZ	SCTFVPTSYHQKCKEETECSSWSSTCNGITTAECPEPRHRDDKIMCNGNTALCIRGECSSGSPCL LWNMIKCFLLTSTT	817	
MKUZ	QCAFKSKS--EKCRDSDCAKEGICNGIFTALCPASDPPKPNFTDCNRHTQVCTINGQCAGSICEKYDLEEC--TCAS	585	
XKUZ	GCTFKRAG--ENCREEEDCAKMGTCNGNSAQCPSPSEPRENLIE-NRATQVCTIKGQCSGSICERYDLEEC--TCGS	109	
DKUZ	LPHVSKRKLGDLACQDGNDISTCRSTISEFADKYNIAQKGGIISLQPGSPCDNFFQGYCDVFLKCRADVADGGPLLRLKN	892	
MKUZ	SDGKDNKELCHVCCMKMAPSTICASTGSLQMSKQFSGRITITLQPGSPCNDFFRGYCDVFMRCRLVDADGPLARLKK	660	
XKUZ	TDEKDDKELCHVCCMEKMIPIHTCASTGSEVWKAYFKGKITITLQPGSPCNEFK	161	
Transmembrane domain			
DKUZ	LLLNRKTLQTVAEWIVDNMYLVLMGVAFIVVMGVSFFIKCCAAVHTPSSNPKKRRARRRISETLRAPMNTLRMRQRHP	967	
MKUZ	AIFSPQLYENIAEWIVAHMVAVLMLGIALIMLMAGFIKICSVHTPSSNPKLPPPKPLPGTLK-----RRRPP	727	
DKUZ	NQRGAGPRRSIPPPAHEAQHYSRGGDGRGGGGGGGRHGGSRSHHQHPHDWRHQGGHSIVPLPTGGSHSSRNSA	1042	
MKUZ	QPIQQPPRRPRESYQMGHMR	749	
DKUZ	ANQARRSDGRPRSTSSGRPQAIIASGSGAASGAARSHGGYGAEAIPGSI GGGVQAAISSGGVVARAQLPLPLPP	1117	
DKUZ	PNGQQQMQQQQLQLQQAISPQQPQAQFYTPKELPPRNKSRSSRTNNTNTTTTNSSTAAGSGSVSGPGSG	1192	
DKUZ	AGSSSKSKSGSAKAKDSKSKSQSQANNSRSSSKEKGVKPVRRNIV	1239	

FIGURE 1A

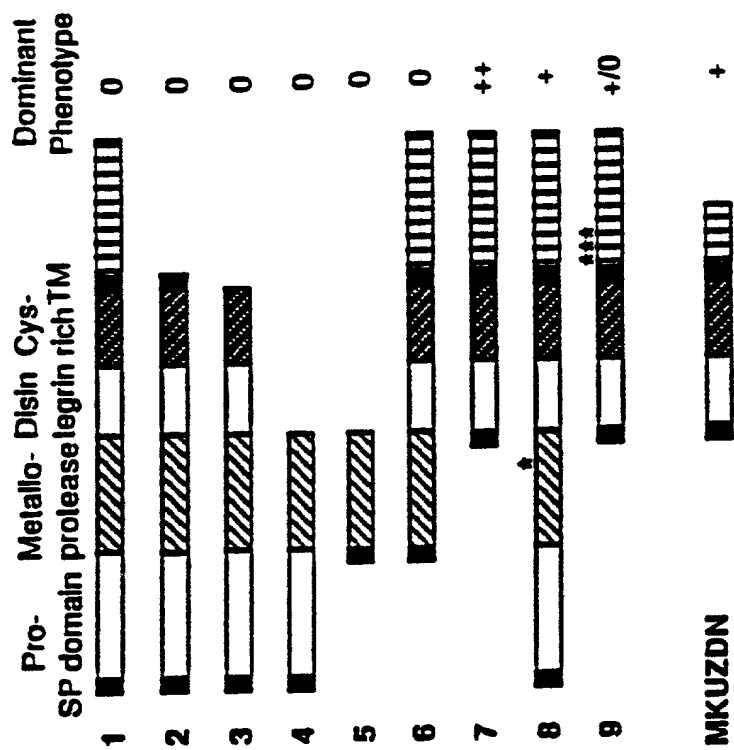
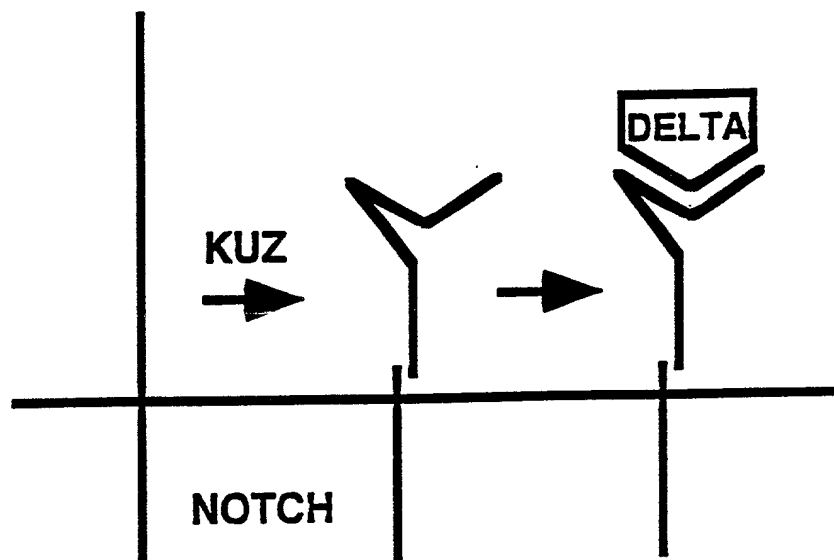


FIGURE 1 B



FIGURE 1 C



**FIGURE 2**